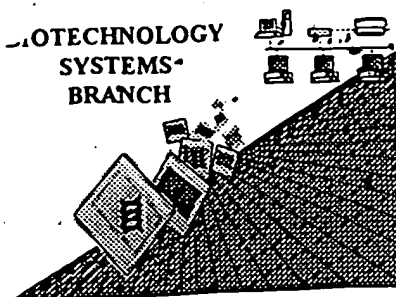


0590
10

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS-
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/816669
Source: OIPE
Date Processed by STIC: 10/04/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/816669

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
 <210> sequence id number
 <400> sequence id number
 000
- 9 ☒ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

may
The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/816,669

DATE: 10/04/2001

TIME: 17:20:41

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10042001\I816669.raw

3 <110> APPLICANT: GARABEDIAN, Michael
 4 TANEJA, Samir
 5 HITTELMAN, Adam
 6 MARKUS, Steven
 8 <120> TITLE OF INVENTION: METHOD FOR SCREENING TRANSCRIPTIONAL COREGULATORY PROTEINS

OF

9 TRANSCRIPTION FACTORS, AND ANDROGEN RECEPTOR TRANSCRIPTIONAL COREGULATORY
 10 PROTEINS AS TARGETS FOR ANDROGEN RECEPTOR-DEPENDENT DISEASES

12 <130> FILE REFERENCE: GARABEDIAN=1.1A

C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/816,669

15 <141> CURRENT FILING DATE: 2001-03-26

17 <150> PRIOR APPLICATION NUMBER: 60/225,618

18 <151> PRIOR FILING DATE: 2000-08-15

20 <150> PRIOR APPLICATION NUMBER: 60/191,768

21 <151> PRIOR FILING DATE: 2000-03-24

23 <160> NUMBER OF SEQ ID NOS: 20

25 <170> SOFTWARE: PatentIn version 3.0

27 <210> SEQ ID NO: 1

28 <211> LENGTH: 474

29 <212> TYPE: DNA

30 <213> ORGANISM: human

32 <400> SEQUENCE: 1

33 atggcgacgc cccctaagcg gcgggcggtg gaggccacgg gggagaaagt gctgcgctac	60
35 gagaccttca tcagtgcgt gctgcagcgg gacttgcgaa aggtgctgga ccatcgagac	120
37 aagggtatatg agcagctggc caaatacctt caactgagaa atgtcattga gcgactccag	180
39 gaagctaagc actcggagtt atatatgcag gtggatttgg gctgtaactt cttcgttgac	240
41 acagtgggtcc cagatacttc acgcatctat gtggccctgg gatatggttt tttcctggag	300
43 ttgacactgg cagaagctct caagttcatt gatcgtgaaga gctctctcct cacagagctc	360
45 agcaacagcc tcaccaagga ctccatgaat atcaaagccc atatccacat gttgctagag	420
47 gggcttagag aactacaagg cctgcagaat ttcccgaga agcctcacca ttga	474

50 <210> SEQ ID NO: 2

51 <211> LENGTH: 157

52 <212> TYPE: PRT

53 <213> ORGANISM: human

55 <400> SEQUENCE: 2

57 Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys	
58 1 5 10 15	
60 Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu	
61 20 25 30	
63 Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys	
64 35 40 45	
66 Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His	
67 50 55 60	
69 Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp	
70 65 70 75 80	
72 Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly	
73 85 90 95	
75 Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg	

Does Not Comply
 Corrected Diskette Needed

Errored: See pages 4 and 5
 and Error Summary Sheet

RAW SEQUENCE LISTING

DATE: 10/04/2001

PATENT APPLICATION: US/09/816,669

TIME: 17:20:41

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10042001\I816669.raw

```

76          100          105          110
78 Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
79          115          120          125
81 Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
82          130          135          140
84 Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
85 145          150          155
87 <210> SEQ ID NO: 3
88 <211> LENGTH: 1097
89 <212> TYPE: DNA
90 <213> ORGANISM: human
92 <400> SEQUENCE: 3
93 aaatgcacaa cccggacgga agtgcctctc cgacagcaga tccaggctcg gagctccaga      60
95 cgctgggaca ggcgcgccgc agaccacccc cgccgcgcgc gggacacgac gccccccgca      120
97 ggacacgccc atcagcccgg aaacccctga gctgcttctc ccggaggccg atgcccaccc      180
99 gggagccccc aaagactcgc ggctcccggg ggcacctgca tactcacccg cctgggcctg      240
101 ggcctccgct gcagggaactg gcgccccgag gcctcaaaac cagcgccccc cgccctccgt      300
103 gccagcccca gccgggaccc cacaaggcaa agaccaagaa gattgtgttt gaggatgagt      360
105 tgctctocca ggccctcctg ggcgccaaga agcctattgg agccatccct aaggggcata      420
107 agcctaggcc ccacccagtg ccgactatg agcttaagta cccgccagtg agcagtgaga      480
109 gggaacggag ccgctatgtc gcagtgttcc aggaccagta cggagagttc ttggagctcc      540
111 agcacgaggt ggggtgtgca caggcaaagc tcaggcagct ggaggccctg ctgagctccc      600
113 tgccccacc ccaaagccag aaggaggccc aagttgcagc ccgggttttg agggagtttg      660
115 agatgaagcg aatggatcct ggcttctctg acaagcaggc tcgctgccac tacctgaagg      720
117 gtaaactgag gcatctcaag actcagatcc agaaattcga tgaccaagga gacagcgagg      780
119 gctccgtgta cttctaagtg cccctgcaga tgggcagagg gatgcatggg gatgcaggtc      840
121 ccttgcatth cttggtatct ctcagctttt cctcttgcat ctccccctac caggggtcgc      900
123 tttctoctgg attgcaaatt cctcttcagt ttggactcag ctctgacagc ccctcctcca      960
125 ggaaggcett ccaggacttc ctcctctggg tcctctagct ctgaccctac agggactcca     1020
127 gatctcaacc tgttcctctg aagtagggcc tgctctccat cccagtgaat taaacatgta     1080
129 ttagacacct aaaaaaa
132 <210> SEQ ID NO: 4
133 <211> LENGTH: 264
134 <212> TYPE: PRT
135 <213> ORGANISM: Human
137 <400> SEQUENCE: 4
139 Met His Asn Pro Asp Gly Ser Ala Ser Pro Thr Ala Asp Pro Gly Ser
140 1          5          10          15
142 Glu Leu Gln Thr Leu Gly Gln Ala Ala Arg Arg Pro Pro Pro Pro Arg
143          20          25          30
145 Ala Gly His Asp Ala Pro Arg Arg Thr Arg Pro Ser Ala Arg Lys Pro
146          35          40          45
148 Leu Ser Cys Phe Ser Arg Arg Pro Met Pro Thr Arg Glu Pro Pro Lys
149          50          55          60
151 Thr Arg Gly Ser Arg Gly His Leu His Thr His Pro Pro Gly Pro Gly
152 65          70          75          80
154 Pro Pro Leu Gln Gly Leu Ala Pro Arg Gly Leu Lys Thr Ser Ala Pro
155          85          90          95
157 Arg Pro Pro Cys Gln Pro Gln Pro Gly Pro His Lys Ala Lys Thr Lys

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/816,669

DATE: 10/04/2001

TIME: 17:20:41

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10042001\I816669.raw

```

158          100          105          110
160 Lys Ile Val Phe Glu Asp Glu Leu Leu Ser Gln Ala Leu Leu Gly Ala
161          115          120          125
163 Lys Lys Pro Ile Gly Ala Ile Pro Lys Gly His Lys Pro Arg Pro His
164          130          135          140
166 Pro Val Pro Asp Tyr Glu Leu Lys Tyr Pro Pro Val Ser Ser Glu Arg
167 145          150          155          160
169 Glu Arg Ser Arg Tyr Val Ala Val Phe Gln Asp Gln Tyr Gly Glu Phe
170          165          170          175
172 Leu Glu Leu Gln His Glu Val Gly Cys Ala Gln Ala Lys Leu Arg Gln
173          180          185          190
175 Leu Glu Ala Leu Leu Ser Ser Leu Pro Pro Pro Gln Ser Gln Lys Glu
176          195          200          205
178 Ala Gln Val Ala Ala Arg Val Trp Arg Glu Phe Glu Met Lys Arg Met
179          210          215          220
181 Asp Pro Gly Phe Leu Asp Lys Gln Ala Arg Cys His Tyr Leu Lys Gly
182 225          230          235          240
184 Lys Leu Arg His Leu Lys Thr Gln Ile Gln Lys Phe Asp Asp Gln Gly
185          245          250          255
187 Asp Ser Glu Gly Ser Val Tyr Phe
188          260

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190 <210> SEQ ID NO: 5

191 <211> LENGTH: 517

192 <212> TYPE: DNA

193 <213> ORGANISM: Human

195 <220> FEATURE:

196 <221> NAME/KEY: misc_feature

197 <223> OTHER INFORMATION: n at position 65 is unknown. *not good*

200 <400> SEQUENCE: 5

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203 cgccgcgag ggagccgagc gcccgmaccg gcccgagcgg acasacgcca gagccgcgcc 120
205 ccgggcccag cgcagcgcgcc cggccgssyg ggccgcccagg ggcgcgcgcg gcggagcgcg 180
207 gggcgcgmgc aaagggggccc ggcggagacc aagggcaggc gcggcccgcg agggcgccgg 240
209 ggaaggcgcc cggcaaggag gcggacaagc ggagcaggcc aacgagacgc gcgcacccac 300
211 acacgagcgc gagccgccac aacaccacac ccggcccaag gagaacagca cgccaacgcg 360
213 ccagycacgg cgggcacggg aggcgggcca cacacagcgg ccccgccaag gcacggcgca 420
215 cggcacaagg gcaccacgcc agacaagcga ggaggcagca cgccgagacc ggccggaggg 480
217 ccgcgaccgc cggagaaaag gaacagagag cccccca 517

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220 <210> SEQ ID NO: 6

221 <211> LENGTH: 189

222 <212> TYPE: PRT

223 <213> ORGANISM: Human

225 <400> SEQUENCE: 6

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227 Glu Phe Gly Thr Arg Ala Arg Phe Thr Arg Gly Lys Ser Ala Leu Leu
228 1          5          10          15
230 Glu Arg Ala Leu Ala Arg Pro Arg Thr Glu Val Ser Leu Ser Ala Phe
231          20          25          30
233 Ala Leu Leu Ser Pro Ser Trp Tyr Ser Thr Ala Arg Ala Val Phe Ser
234          35          40          45

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/816,669

DATE: 10/04/2001

TIME: 17:20:41

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10042001\I816669.raw

```

236 Val Ala Glu Leu Gln Ser Arg Leu Ala Ala Leu Gly Arg Gln Val Gly
237      50                      55                      60
239 Ala Arg Val Leu Asp Ala Leu Val Ala Arg Glu Lys Gly Ala Arg Arg
240 65                      70                      75                      80
242 Glu Thr Lys Val Leu Gly Ala Leu Leu Phe Val Lys Gly Ala Val Trp
243                      85                      90                      95
245 Lys Ala Leu Phe Gly Lys Glu Ala Asp Lys Leu Glu Gln Ala Asn Asp
246                      100                      105                      110
248 Asp Ala Arg Thr Phe Tyr Ile Ile Glu Arg Glu Pro Leu Ile Asn Thr
249                      115                      120                      125
251 Tyr Ile Ser Val Pro Lys Glu Asn Ser Thr Leu Asn Cys Ala Ser Phe
252      130                      135                      140
254 Thr Ala Gly Ile Val Glu Ala Val Leu Thr His Ser Gly Phe Pro Ala
255 145                      150                      155                      160
257 Lys Val Thr Ala His Trp His Lys Gly Thr Thr Leu Met Ile Lys Phe
258                      165                      170                      175
260 Glu Glu Ala Val Ile Ala Arg Asp Arg Leu Glu Gly Arg
261                      180                      185
263 <210> SEQ ID NO: 7
264 <211> LENGTH: 126
265 <212> TYPE: DNA
266 <213> ORGANISM: Human
268 <400> SEQUENCE: 7
269 gaattcggca cgaggctcaa gccctacgtg agctacctcg cccctgagag cgaggagacg      60
271 cccctgacgg ccgcgcagct cttcagcaag ccgttggcgc cttgccatcg aaaaggactt      120
273 caagga      126
276 <210> SEQ ID NO: 8
277 <211> LENGTH: 42
278 <212> TYPE: PRT
279 <213> ORGANISM: Human
281 <400> SEQUENCE: 8
283 Glu Phe Gly Thr Arg Leu Lys Pro Tyr Val Ser Tyr Leu Ala Pro Glu
284 1                      5                      10                      15
286 Ser Glu Glu Thr Pro Leu Thr Ala Ala Gln Leu Phe Ser Lys Pro Leu
287      20                      25                      30
289 Ala Pro Cys His Arg Lys Gly Leu Gln Gly
290      35                      40
292 <210> SEQ ID NO: 9
293 <211> LENGTH: 678
294 <212> TYPE: DNA
295 <213> ORGANISM: Human
297 <220> FEATURE:
298 <221> NAME/KEY: misc_feature
299 <223> OTHER INFORMATION: n at position 651 is unknown. -- need to include reference
302 <400> SEQUENCE: 9
303 gaattcggca cgaggattca ttgccccac aatcctaggc ctaccgcgcg cagtactgat      60
305 cattctatct cccctctat tgatccccac ctccaaatat ctcataaca accgactaat      120
307 caccacccaa caatgactaa tcaaactaac ctcaaaacaa atgataacca tacacaacac      180
309 taaaggacga acctgatctc ttatactagt atccttaatc atttttattg ccacaactaa      240

```

Errored
 to position 657. - need to include reference

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 10/04/2001

PATENT APPLICATION: US/09/816,669

TIME: 17:20:42

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10042001\I816669.raw

311 cctcctcgga ctctgcctc actcatttac accaaccacc caactatcta taaacctagc 300
 313 catggccatc ccttatgag cgggcgcagt gattataggc tttcgctcta agattaaaaa 360
 315 tgccttagcc cactttctac cacaaggcac acctacaccc cttatcccca tactagttat 420
 317 tatcgaaacc atcagcctac tcattcaacc aatagccctg gccgtacgcc taaccgctaa 480
 319 cattactgca ggccacctac tcatgcacct aattggaagc gccaccctag caatatcaac 540
 321 cattaacctt cctctacact tatcatcttc acaattctaa ttctactgac tctctagaa 600
 W--> 323 atcgctgtcg ccttaatcca agcctacgtt ttcacacttc tagtaagcct ~~ttactgacg~~ 660
 325 acaacacata aaaaaaaa 678
 328 <210> SEQ ID NO: 10
 329 <211> LENGTH: 60
 330 <212> TYPE: PRT
 331 <213> ORGANISM: Human
 333 <400> SEQUENCE: 10
 335 Glu Phe Gly Thr Arg Ile His Cys Pro His Asn Pro Arg Pro Thr Arg
 336 1 5 10 15
 338 Arg Ser Thr Asp His Ser Ile Ser Pro Ser Ile Asp Pro His Leu Gln
 339 20 25 30
 341 Ile Ser His Gln Gln Pro Thr Asn His His Pro Thr Met Thr Asn Gln
 342 35 40 45
 344 Thr Asn Leu Lys Thr Asn Asp Asn His Thr Gln His
 345 50 55 60
 347 <210> SEQ ID NO: 11
 348 <211> LENGTH: 1918
 349 <212> TYPE: DNA
 350 <213> ORGANISM: Human
 352 <400> SEQUENCE: 11
 353 gaattccaat gtggttaaagt cttcgctcaa acatcacaac ttgcaaggca ttggagagtt 60
 355 catactggag aaaaacctta caagtgtaat gactgtggca gagccttttag tgatcgttca 120
 357 agcctaactt ttcacagggc aatacatact ggagagaaac cttacaaatg tcatgaatgc 180
 359 ggcaagggtt ttaggcacaa ttcatacctt gcaactcatc ggcaattca tactggagag 240
 361 aaaccttaca agtgtaatga gtgtgggaaa gccttttagta tgcattcaaa cctaactacc 300
 363 cataagggtca tccatactgg agagaagcct taaaaatgta atcaatgtgg caaggtcttc 360
 365 actcagaact cacaccttgc aaatcatcaa aggactcaca ccggagagaa acctaccga 420
 367 tgcaatgagt gtgggaaagc cttcagtgtt cgttcaagcc taaccaccca tcaggcaatc 480
 369 catactggga aaaaacctta caaatgtaat gaatgtggca aggtctttac tcaaaatgct 540
 371 cacctggcaa atcaccgaag aattcatact ggggagaac cttacaggtg tacagagtgt 600
 373 gggaaagcct ttagggtaag atcaagtcta actaccata tggcaatcca cactggagaa 660
 375 aagcgttaca aatgtaatga gtgtggcaag gtcttcaggc agagttcaaa tcttgcaagt 720
 377 catcacagaa tgcataccgg agagaaacct taaaaatgag tgtggtgagg tcattaggtg 780
 379 caattcactc ctttcacatc agttaatttc attcttgaca gaatccttac aaatgtagtg 840
 381 acagtggcca atccctcatg agttgaagca ttaatatgata tgagaggcca taagcaagag 900
 383 acatcatgta aacatatgtg gcagagggtc tatccaggcc tcgcagggtta ctaggcatca 960
 385 agatttatat ctttgatgaa acgaaacaaa tgtaatatgc atcctgaggc cattaccag 1020
 387 tgaccgatgg taagtgagga ttcctaggag gaataacagt ctctggtttc cctggtttgcc 1080
 389 tttgatatta tacactgtag aatactcaca agtccaaata tgctaaaaat tatatatatt 1140
 391 taactcacat acgaaaagg tgcaggatat ttgtaggcag tcagttacct tcaccttatg 1200
 393 aaatgtttca ctgagttatt tgaggttttt tggaaagcct actattgcgt ttcaatgtga 1260
 395 actttgaaat cttattgtgc atccttacac acctccatg gtgctttctt ggaaagatca 1320
 397 ttgggatgga aggatcattg attgggtgaa gatcattgat taggtgaagg attatttcta 1380

Errored: Unknown at
 location 657 is not
 identified in fields 221 or 223.

FYI: "Artificial Sequence" is the preferred
 field 213 term as opposed to "Artificial".

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/816,669

DATE: 10/04/2001

TIME: 17:20:43

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10042001\I816669.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:203 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:323 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1324 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:1336 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:1348 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:1360 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:1372 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:1384 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20